

## SEQUENCE LISTING

<110> Chadwick, Brian Paul  
Frischauf, Anna-Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
POLYPEPTIDES AND NUCLEIC ACIDS

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<141> 1999-01-29

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<170> PatentIn Ver. 2.0

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Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Thr Pro Val Val			
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cta aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag	672		
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys			
130	135	140	
gct ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg	720		
Ala Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu			
145	150	155	
gta cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata	768		
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile			
160	165	170	
tta gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac	816		
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His			
175	180	185	190
aga cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa	864		
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln			
195	200	205	
atc acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg	912		
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg			
210	215	220	
ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat	960		
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr			
225	230	235	
aca cat agt tac ttg gga ttt gga ttg aaa gct gca aga cta gca acc	1008		
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr			
240	245	250	
ctg gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt	1056		
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser			
255	260	265	270
gcc tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg	1104		
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val			
275	280	285	
aaa tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc	1152		
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro			
290	295	300	
tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca	1200		
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro			
305	310	315	
gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac	1248		
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp			
320	325	330	

cga gct gtt gac aca gac atg att gat tat gaa aag	ggg ggt att tta	1296	
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys	Gly Gly Ile Leu		
335	340	345	350
aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg	tgt gat aac ttg	1344	
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	Cys Asp Asn Leu		
355	360	365	
gaa aac ttc acc tca ggc agt cct ttc ctg tgc atg	gat ctc agc tac	1392	
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met	Asp Leu Ser Tyr		
370	375	380	
atc aca gcc ctg tta aag gat ggc ttt ggc	ttt gca gac agc aca gtc	1440	
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala	Asp Ser Thr Val		
385	390	395	
tta cag ctc aca aag aaa gtg aac aac ata gag acg	ggc tgg gcc ttg	1488	
Gly Ala Leu Thr Lys Lys Val Asn Asn Ile Glu	Trp Ala Leu		
400	405	410	
ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc	tcc cat	1530	
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile	Ser His		
415	420	425	
tgaggccacg tacttccttg gagacctgca ttggcaaca	ccttttaag gggaggagag	1590	
agcacttagt ttctgaacta gtctggaca tcctggactt	gagcctagag atttagttt	1650	
aattaatttt acacatctaa tgtgaactgc tgcctaacc	ctcaagagta cacagctggc	1710	
accagagcat cacagagagc cctgtgagcc	aaaaagtata gtttggAAC ttaaccttgg	1770	
agtgagagcc caggagcagg tccctggaaa ccaaagaaaa	atcgatttc aacccttga	1830	
gtgcctcatt ccactgaata tttaaatttt cctcttaaat	gttaaactga cttattgcaa	1890	
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 <212> PRT  
 <213> Homo sapiens

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20	25	30	
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val	Ser Ala Ser Thr Leu		
35	40	45	
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly	Thr Arg Ile His Val		
50	55	60	

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
 65 70 75 80  
 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
 85 90 95  
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
 100 105 110  
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
 115 120 125  
 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
 130 135 140  
 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro  
 145 150 155 160  
 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala  
 165 170 175  
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln  
 180 185 190  
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr  
 195 200 205  
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr  
 210 215 220  
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His  
 225 230 235 240  
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly  
 245 250 255  
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys  
 260 265 270  
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr  
 275 280 285  
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr  
 290 295 300  
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu  
 305 310 315 320  
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala  
 325 330 335  
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val  
 340 345 350  
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn  
 355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr  
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Ala Asp Ser Thr Val Leu Gln  
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala  
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His  
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<211> 2119

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (205)..(1599)

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atgtgctttt taaattggcc tgcgtgaccc gcccacttgg tggaaaagaa gaaccggcca 120

aaggggggc ctgaaggacc tccacaggag tggtagcgcg actgtcttcag caacaagcc 180

tcaggtccac atcttggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231  
Met Ala Thr Ser Trp Gly Ala Val Phe  
1 5

atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279  
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln  
10 15 20 25

cag acc tgg ttt gaa ggt gtc ttc ttg tct tcc atg tgc ccc att aat 327  
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn  
30 35 40

gtc agt gcc ggc acc ttt tat gga att atg ttt gat gcg ggc agc act 375  
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr  
45 50 55

gga gct cgg att cat gtt tac act ttt gtg cag aaa aca gca gga cag 423  
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln  
60 65 70

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt 471  
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu  
75 80 85

tct gct ttt gtg gat cag ccc aaa cag ggt gct gag act gtc cag gag 519  
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu  
90 95 100 105

ctc ttg gag gtg gcc aaa gac tcg atc ccc aga agc cac tgg gaa agg	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
acc ccg gtg gtt ctg aaa gca acg gcc gga ctc cgt ttg ctg cct gag	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
cag aaa gcc cag gct ctg ctc ttg gag gta gag gag atc ttc aag aat	663
Gln Lys Ala Glu Ala Leu Leu Glu Val Glu Glu Phe Lys Asn	
140 145 150	
tca cct ttc ctg gtc cca gat ggc agc gtt agc atc atg gat ggg tcc	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	
tat gaa ggc ata cta gcc tgg gtt acc gtc aac ttt cta aca ggt cag	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	
170 175 180 185	
ctg cat ggt cgt ggc cag gag act gtc ggg acc ctt gac ctg ggg ggt	807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	
190 195 200	
gcc tcc acc caa atc acg ttt cta ccc cag ttt gag aaa acc ctg gaa	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	
205 210 215	
caa aca cct agg ggc tac ctc act tcc ttt gag atg ttt aac agc act	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	
220 225 230	
ttt aag ctc tat aca cat agt tac ttg gga ttt gga ctg aaa gct gca	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	
235 240 245	
aga ctg gca act ctg gga gcc gca aaa ggg act gat gga cat	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	
250 255 260 265	
acg ttt cga agt gcc tgt tta cca aga tgg ttg gaa gca gag tgg atc	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	
270 275 280	
ttt ggg ggt gtg aaa tac cag tat ggt ggt aac caa gaa ggg gag atg	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met	
285 290 295	
ggc ttt gaa ccc tgc tat gcg gaa gtg ctg agg gta gta cag ggg aaa	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	
300 305 310	
ctt cac cag cca gaa gaa gtc cga gga agc gcc ttc tac gct ttc tct	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	
315 320 325	

tac tac tac gat cga gcc gct gac aca cac ttg atc gat tat gaa aag	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	
330 335 340 345	
ggc ggg gtt tta aaa gtt gaa gat ttt gaa aga aaa gcc aga gaa gtg	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	
350 355 360	
tgt gac aac ttg ggg agc ttc tcc tcg ggc agt cct ttc ctc tgc atg	1335
Cys Asp Asn Leu Gly Ser Phe Ser Gly Ser Pro Phe Leu Cys Met	
365 370 375	
gac ctc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	
380 385 390	
gaa cgg cac cct ctt aca gct cac aaa gaa agt gaa caa cat aga gac	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	
395 400 405	
tgg ttg ggc ctt ggg ggc cac ctt tca cct gct cca gtc tct ggg cat	1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His	
410 415 420 425	
cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	
430 435 440	
gtt ttc tca cag gaa ggc gtg gac tca gag aca ttt tct gac ctc tct	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	
445 450 455	
gga aaa gcc tgg ccc gaa acc cgt taactggttt tataaggagg gagggggttt	1629
Gly Lys Ala Trp Pro Glu Thr Arg	
460 465	
tagatgagtc ttgctttga gcctagtgtat ttgggcttca atgatttgc aatctaattgt	1689
gaatagtc taaccacttg gtgggtgcat ggctggcacc agactgtaaa tctttggga	1749
ttctttgtac agagtcgtc aaaggaaaaa agagaaaaagg tttggactc catgttagat	1809
tgcgagttca gagacaggtc cctggggacc aaagaacaat ctcgtttcaa cccttggatg	1869
cctcattgtc ttgaatggat tcattttgc ttataagctg atttactgaa atcccataac	1929
ccatcaatgc tgtaatttt ttcttctca cccttattac atcccttacc ctaaaagct	1989
ggggaaata cctgggtttt ctccccatct ataattgaga aagagggggg aaaagatact	2049
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aaaaaaaaaa	2119
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<213> Mus musculus

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Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val  
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Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr  
35 40 45  
Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr  
50 55 60  
Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu  
65 70 75 80  
Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro  
85 90 95  
Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp  
100 105 110  
Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala  
115 120 125  
Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu  
130 135 140  
Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp  
145 150 155 160  
Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp  
165 170 175  
Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu  
180 185 190  
Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe  
195 200 205  
Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu  
210 215 220  
Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser  
225 230 235 240  
Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala  
245 250 255  
Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu  
260 265 270  
Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln  
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala  
 290 295 300  
 Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val  
 305 310 315 320  
 Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala  
 325 330 335  
 Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu  
 340 345 350  
 Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe  
 355 360 365  
 Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala  
 370 375 380  
 Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala  
 385 390 395 400  
 His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly His  
 405 410 415  
 Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser  
 420 425 430  
 Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val  
 435 440 445  
 Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr  
 450 455 460  
 Arg  
 465  
  
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 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
 35 40 45  
 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
 50 55 60  
 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
 65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
                   85                  90                  95  
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
                   100              105              110  
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
                   115              120              125  
 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
                   130              135              140  
 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro  
                   145              150              155              160  
 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala  
                   165              170              175  
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln  
                   180              185              190  
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr  
                   195              200              205  
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr  
                   210              215              220  
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His  
                   225              230              235              240  
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly  
                   245              250              255  
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys  
                   260              265              270  
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr  
                   275              280              285  
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr  
                   290              295              300  
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu  
                   305              310              315              320  
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala  
                   325              330              335  
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val  
                   340              345              350  
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn  
                   355              360              365  
 Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr  
                   370              375              380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln  
385 390 395 400

Leu Thr Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala  
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His  
420 425

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<212> PRT  
<213> P. sativum

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20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe  
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln  
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys  
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala  
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp  
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu  
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg  
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val  
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val  
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly  
180 185 190

Val Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser  
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro  
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val  
 225 230 235 240  
 His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu  
 245 250 255  
 Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn  
 260 265 270  
 Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr  
 275 280 285  
 Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu  
 290 295 300  
 Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile  
 305 310 315 320  
 Trp Asn Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser  
 325 330 335  
 Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr  
 340 345 350  
 Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu  
 355 360 365  
 Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu  
 370 375 380  
 Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln  
 385 390 395 400  
 Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile  
 405 410 415  
 Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala  
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 435 440 445  
 Glu Arg Leu Met Tyr Phe Val  
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 <211> 454  
 <212> PRT  
 <213> Solanum tuberosum

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 Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile  
 20 25 30

Pro	Leu	Arg	Arg	His	Leu	Leu	Ser	His	Glu	Ser	Glu	His	Tyr	Ala	Val
35								40				45			
Ile	Phe	Asp	Ala	Gly	Ser	Thr	Gly	Ser	Arg	Val	His	Val	Phe	Arg	Phe
50							55				60				
Asp	Glu	Lys	Leu	Gly	Leu	Leu	Pro	Ile	Gly	Asn	Asn	Ile	Glu	Tyr	Phe
65							70			75			80		
Met	Ala	Thr	Glu	Pro	Gly	Leu	Ser	Ser	Tyr	Ala	Glu	Asp	Pro	Lys	Ala
85							90			95					
Ala	Ala	Asn	Ser	Leu	Glu	Pro	Leu	Leu	Asp	Gly	Ala	Glu	Gly	Val	Val
100							105				110				
Pro	Gln	Glu	Leu	Gln	Ser	Glu	Thr	Pro	Leu	Glu	Leu	Gly	Ala	Thr	Ala
115							120				125				
Gly	Leu	Arg	Met	Leu	Lys	Gly	Asp	Ala	Ala	Glu	Lys	Ile	Leu	Gln	Ala
130							135			140					
Val	Arg	Asn	Leu	Val	Lys	Asn	Gln	Ser	Thr	Phe	His	Ser	Lys	Asp	Gln
145							150			155			160		
Trp	Val	Thr	Ile	Leu	Asp	Gly	Thr	Gln	Glu	Gly	Ser	Tyr	Met	Trp	Ala
165							170				175				
Ala	Ile	Asn	Tyr	Leu	Leu	Gly	Asn	Leu	Gly	Lys	Asp	Tyr	Lys	Ser	Thr
180							185				190				
Thr	Ala	Thr	Ile	Asp	Leu	Gly	Gly	Ser	Val	Gln	Met	Ala	Tyr	Ala	
195							200			205					
Ile	Ser	Asn	Glu	Gln	Phe	Ala	Lys	Ala	Pro	Gln	Asn	Glu	Asp	Gly	Glu
210							215			220					
Pro	Tyr	Val	Gln	Gln	Lys	His	Leu	Met	Ser	Lys	Asp	Tyr	Asn	Leu	Tyr
225							230			235			240		
Val	His	Ser	Tyr	Leu	Asn	Tyr	Gly	Gln	Leu	Ala	Gly	Arg	Ala	Glu	Ile
245							250			255					
Phe	Lys	Ala	Ser	Arg	Asn	Glu	Ser	Asn	Pro	Cys	Ala	Leu	Glu	Gly	Cys
260							265			270					
Asp	Gly	Tyr	Tyr	Ser	Tyr	Gly	Gly	Val	Asp	Tyr	Lys	Val	Lys	Ala	Pro
275							280				285				
Lys	Lys	Gly	Ser	Ser	Trp	Lys	Arg	Cys	Arg	Arg	Leu	Thr	Arg	His	Ala
290							295			300					
Leu	Lys	Ile	Asn	Ala	Lys	Cys	Asn	Ile	Glu	Glu	Cys	Thr	Phe	Asn	Gly
305							310			315			320		
Val	Trp	Asn	Gly	Gly	Gly	Asp	Gly	Gln	Lys	Asn	Ile	His	Ala	Ser	
325							330			335					

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys  
 340 345 350  
 Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys  
 355 360 365  
 Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys  
 370 375 380  
 Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu  
 385 390 395 400  
 Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile  
 405 410 415  
 Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala  
 420 425 430  
 Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys  
 435 440 445  
 Ile Arg Val Ala Ser Ser  
 450

<210> 12  
 <211> 473  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 12  
 Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly  
 1 5 10 15

Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp  
 20 25 30

Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr  
 35 40 45

Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr  
 50 55 60

Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe  
 65 70 75 80

Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly  
 85 90 95

Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val  
 100 105 110

Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala  
 115 120 125

Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala  
 130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly  
 145 150 155 160  
 Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp  
 165 170 175  
 Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys  
 180 185 190  
 Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Ser Thr Gln Ile  
 195 200 205  
 Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu  
 210 215 220  
 His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln  
 225 230 235 240  
 Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn  
 245 250 255  
 Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys  
 260 265 270  
 Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val  
 275 280 285  
 Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr  
 290 295 300  
 Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe  
 305 310 315 320  
 Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro  
 325 330 335  
 Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys  
 340 345 350  
 Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr  
 355 360 365  
 Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp  
 370 375 380  
 Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe  
 385 390 , 395 400  
 Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe  
 405 410 415  
 Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp  
 420 425 430  
 Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys  
 435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp  
450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala  
465 470

<210> 13  
<211> 153  
<212> PRT  
<213> Homo sapiens

<400> 13  
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr  
1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His  
20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val  
35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg  
50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr  
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu  
85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr  
100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly  
115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln  
130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro  
145 150

<210> 14  
<211> 154  
<212> PRT  
<213> Rattus norvegicus

<400> 14  
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu  
1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr  
35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys  
 50 55 60  
 Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val  
 65 70 75 80  
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys  
 85 90 95  
 Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser  
 100 105 110  
 Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu  
 115 120 125  
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr  
 130 135 140  
 Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser  
 145 150

<210> 15  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe  
 1 5 10 15  
 Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly  
 20 25 30  
 Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala  
 35 40 45  
 Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln  
 50 55 60  
 Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr  
 65 70 75 80  
 Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu  
 85 90 95  
 Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr  
 100 105 110  
 Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly  
 115 120 125  
 Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys  
 130 135 140  
 Tyr Gly Trp Val Gly Arg Trp Phe Arg  
 145 150

<210> 16  
<211> 150  
<212> PRT  
<213> Gallus gallus

<400> 16  
Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val  
1 5 10 15  
Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val  
20 25 30  
Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr  
35 40 45  
Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser  
50 55 60  
Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu  
65 70 75 80  
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro  
85 90 95  
Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr  
100 105 110  
Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly  
115 120 125  
Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys  
130 135 140  
Arg Gly Trp Leu Gly Glu  
145 150

<210> 17  
<211> 148  
<212> PRT  
<213> Caenorhabditis elegans

<400> 17  
Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu  
1 5 10 15  
Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp  
20 25 30  
Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly  
35 40 45  
Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr  
50 55 60  
Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly  
65 70 75 80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro  
85 90 95  
Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys  
100 105 110  
Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp  
115 120 125  
Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu  
130 135 140  
Gly Arg Phe Asp  
145

<210> 18  
<211> 10  
<212> RNA  
<213> Mus musculus

<400> 18  
aagaaauagg

10

<210> 19  
<211> 10  
<212> RNA  
<213> Vertebrate

<400> 19  
ggcgcccaugg

10

<210> 20  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20  
ccagactgta aatcttttgg

20

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21  
aggaaatgta ataagggtag

20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 22  
ctgcgttgagt gacgtctctg 20

<210> 23  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 23  
cacatgaggt tcagctcgta 20

<210> 24  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
gtgaagtggc tgccttcagg 20

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
cctttgactc gggactccagg 20

<210> 26  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
gaactgctgc ctaaccactc 20

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
attgatgggt cttgggattg c 21

<210> 28  
<211> 10  
<212> RNA  
<213> Homo sapiens

<400> 28  
augugaauga 10

<210> 29  
<211> 10  
<212> RNA  
<213> Homo sapiens

<400> 29  
acaaggaauga 10